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DATE: Thursday, September 22, 2005

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<input type="checkbox"/>	L2	nadp same dependent same glyceraldehyde same phosphate same dehydrogenase	35
<input type="checkbox"/>	L1	nadp same dependent same glyceraldehyde same phosphate same dehydrogenase	0

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Set	Items	Description
S1	158230	GROUP(W)B OR STREPTOCOCCUS(W)AGALCTIAE OR S(W)AGALACTIAE
S2	46	S1 AND (GLYCERALDEHYDE AND PHOSPHATE AND DEHYDROGENASE)
S3	19	RD S2 (unique items)

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Search in ENZYME for: NADp dependent glyceraldehyde phosphate dehydrogenase

Release 38, September 2005, and updates up to 13-Sep-2005

Please choose one of the following entries:

- 1.2.1.13 Glyceraldehyde-3-phosphate dehydrogenase (NADP(+)) (phosphorylating).
 (AN: NADP-dependent glyceraldehyde-3-phosphate dehydrogenase.
 Triosephosphate dehydrogenase (NADP(+)).
 Triosephosphate dehydrogenase (NADP+).)

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0013603725 BIOSIS NO.: 200200197236

Identification of major outer surface proteins of *Streptococcus agalactiae*

AUTHOR: Hughes Martin J G (Reprint); Moore Joanne C; Lane Jonathan D; Wilson Rebecca; Pribul Philippa K; Younes Zabin N; Dobson Richard J; Everest Paul; Reason Andrew J; Redfern Joanne M; Greer Fiona M; Paxton Thanai; Panico Maria; Morris Howard R; Feldman Robert G; Santangelo Joseph D

AUTHOR ADDRESS: 545 Eskdale Rd., Winnersh Triangle, Wokingham, Berks, RG41 5TU, UK**UK

JOURNAL: Infection and Immunity 70 (3): p1254-1259 March, 2002 2002

MEDIUM: print

ISSN: 0019-9567

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: To identify the major outer surface proteins of *Streptococcus agalactiae* (**group B streptococcus**), a proteomic analysis was undertaken. An extract of the outer surface proteins was separated by two-dimensional electrophoresis. The visualized spots were identified through a combination of peptide sequencing and reverse genetic methodologies. Of the 30 major spots identified as ***S***, ***agalactiae*** specific, 27 have been identified. Six of these proteins, previously unidentified in ***S***, ***agalactiae***, were sequenced and cloned. These were ornithine carbamoyltransferase, phosphoglycerate kinase, nonphosphorylating **glyceraldehyde-3-phosphate dehydrogenase**, purine nucleoside phosphorylase, enolase, and glucose-6-***phosphate*** isomerase. Using a gram-positive expression system, we have overexpressed two of these proteins in an in vitro system. These recombinant, purified proteins were used to raise antisera. The identification of these proteins as residing on the outer surface was confirmed by the ability of the antisera to react against whole, live bacteria. Further, in a neonatal-animal model system, we demonstrate that some of these sera are protective against lethal doses of bacteria. These studies demonstrate the successful application of proteomics as a technique for identifying vaccine candidates.

0014496996 BIOSIS NO.: 200300455675

Characterization of **group B streptococcal glyceraldehyde**
-3-phosphate dehydrogenase: Surface localization, enzymatic
activity, and protein-protein interactions.

AUTHOR: Seifert Kyle N; McArthur William P; Bleiweis Arnold S; Brady L
Jeannine (Reprint)

AUTHOR ADDRESS: Department of Oral Biology, College of Dentistry,
University of Florida, Gainesville, FL, 32610-0424, USA**USA

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JOURNAL: Canadian Journal of Microbiology 49 (5): p350-356 May 2003 2003

MEDIUM: print

ISSN: 0008-4166

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: During characterization of the surface antigens of serotype III
group B streptococci (GBS), a protein with an apparent
Mrapprx173 500 migrating on a SDS - polyacrylamide gel was found to have
an N-terminal amino acid sequence identical to that of the plasmin
receptor (Plr) of group A streptococci, a surface-localized
glyceraldehyde -3- ***phosphate*** ***dehydrogenase*** (GAPDH).

This

work begins to characterize GBS GAPDH and to assess its functional
activity on the cell surface. The 1.0-kb gapC gene of GBS was amplified
by PCR. plr and gapC demonstrated 87% homology. An anti-Plr monoclonal
antibody reacted with GBS whole cells, suggesting GBS GAPDH is surface
localized. Multiple serotypes of GBS demonstrated functional GAPDH on
their surfaces. The anti-Plr monoclonal antibody recognized GBS protein
bands of approximately 41 and 173.5 kDa, by Western blot. Presumably,
these represent monomeric and tetrameric forms of the GAPDH molecule. GBS
GAPDH was demonstrated by Western blot analysis to interact with lys- and
glu-plasminogens. Fluid-phase GBS GAPDH interacted, by means of ELISA,
with immobilized lys-plasminogen, glu-plasminogen, actin, and fibrinogen.
Enzymatically active GAPDH, capable of binding cytoskeletal and
extracellular matrix proteins, is expressed on the surface of GBS.

0014564481 BIOSIS NO.: 200300519844

Oxygen regulates invasiveness of ***group*** ***B*** Streptococcus.

AUTHOR: Johri A K (Reprint); Padilla J (Reprint); Malin G (Reprint);

Paoletti L C (Reprint)

AUTHOR ADDRESS: Brigham and Women's Hosp., Harvard Med. Sch., Boston, MA,
USA**USA

JOURNAL: Abstracts of the General Meeting of the American Society for
Microbiology 103 pB-090 2003 2003

MEDIUM: cd-rom

CONFERENCE/MEETING: 103rd American Society for Microbiology General Meeting
Washington, DC, USA May 18-22, 2003; 20030518

SPONSOR: American Society for Microbiology

ISSN: 1060-2011 (ISSN print)

DOCUMENT TYPE: Meeting; Meeting Abstract

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Group B Streptococcus (GBS) is a member of the normal human colonic microflora that can colonize the vagina and rectum asymptotically. GBS also can cause pneumonia, sepsis, and meningitis among newborns; endometritis and other illnesses among peripartum women; and skin and soft-tissue infections in the elderly. Although several virulence factors have been identified, environmental conditions responsible for the transition of GBS from a commensal to a pathogen have not been delineated. Previous studies with our newly developed dynamic in vitro attachment and invasion system (DIVAS) showed that GBS organisms invade respiratory epithelial cells most effectively when held at a fast cell mass doubling time (td) of 1.8 h as opposed to a slower td of 11 h. For those studies, GBS were grown in continuous culture in a chemically defined medium with glucose limitation in the presence of added air. Herein we sought to determine whether oxygen influenced the ability of GBS to invade epithelial cells in vitro. When held at the invasive (td=1.8 h) condition in DIVAS, GBS invaded epithelial cells in significantly greater numbers when grown with dissolved oxygen (DO₂) levels of >5% than when grown in the absence of DO₂. A pulse of oxygen (DO₂ of 0.1% to 2.7%) during the 2-h invasion period resulted in a greater number of invasive GBS compared to the number obtained when GBS was grown with 0.3% DO₂. Thus, only brief exposure to oxygen may be sufficient to upregulate components necessary for invasion by GBS, which is a facultative anaerobe. Oxygen-regulated invasion by GBS was observed with immortalized human epithelial cells from lungs, cervix, vagina, endometrium, and primitive neurons. Cell envelope proteins from GBS expressed either predominantly or solely at the invasive growth condition were isolated and partial sequences determined by nanoelectrospray tandem mass spectrometry. Three of these proteins revealed homologies with sequences for GBS proteins: FhuD, **glyceraldehyde-3-phosphate** ***dehydrogenase***, and chaperonin 60 kDa. These proteins may be important for GBS invasiveness and also may be targets for vaccine development.

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L2: Entry 4 of 35

File: PGPB

May 19, 2005

DOCUMENT-IDENTIFIER: US 20050106734 A1

TITLE: Fungal micro-organism having an increased ability to carry out biotechnological process(es)

Detail Description Paragraph:

[0028] Glyceraldehyde 3-phosphate dehydrogenases (GAPDH) are known as non-phosphorylating enzymes (GAPN, EC 1.2.1.8) and phosphorylating enzymes. For the phosphorylating enzymes nicotinamide dinucleotide (NAD) dependent enzymes (NAD-GAPDH, EC 1.2.1.12) and nicotinamide dinucleotide phosphate (NADP) dependent enzymes (NADP-GAPDH, EC 1.2.1.13) are known. The NAD-GAPDH is a glycolytic enzyme, which is highly conserved in prokaryotes and eukaryotes. NADP-GAPDH is known in bacteria (e.g. Koksharova et al. 1998, Fillinger et al. 2000). For plants an NADP-GAPDH, which is involved in the photosynthetic CO₂ assimilation and located in the chloroplasts, is known (Cerff 1982). The NADP-GAPDH of chloroplasts has the two subunits A and B (Shih et al. 1991, Baalman et al. 1996). Other eukaryotic NADP-GAPDH are not known.

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L2: Entry 8 of 35

File: PGPB

Feb 12, 2004

DOCUMENT-IDENTIFIER: US 20040029118 A1

TITLE: Streptococcus pneumoniae polynucleotides and sequences

Detail Description Table CWU:

181 8 4033 5751 gi.vertline.149411 enzyme III [Lactococcus lactis] 89 80 1719 211 4
 3149 2793 gi.vertline.535273 aminopeptidase C 89 83 357 [Streptococcus
 thermophilus] 361 1 431 838 gi.vertline.1196922 unknown protein [Insertion 89 70
 408 sequence IS861] 34 17 11839 10535 sp.vertline.P30053.vertline.SYH_S HISTIDYL-
 TRNA SYNTHETASE 88 78 1305 (EC 6.1 1.21) (HISTIDINE-- TRNA LIGASE) (HISRS). 38 3
 1646 2623 gi.vertline.2058544 putative ABC transporter 88 78 978 subunit ComYA
 [Streptococcus gordonii] 54 1 3 227 gnl.vertline.PID.vertline.d101320 YqgU
 [Bacillus subtilis] 88 66 225 57 2 611 1468 gnl.vertline.PID.vertline.e134943
 putative reductase 1 88 75 858 [Saccharomyces cerevisiae] 65 13 5497 6069
 pir.vertline.A29102.vertline.R5BS ribosomal protein L5 - 88 75 573 Bacillus
 stearothermophilus 65 20 9030 9500 gi.vertline.2078381 ribosomal protein L15 88 83
 471 [Staphylococcus aureus] 78 3 3636 1108 gnl.vertline.PID.vertline.d- 100781
 lysyl-aminopeptidase 88 80 2529 [Lactococcus lactis] 106 12 12965 12054
 gi.vertline.2407215 (AF017421) putative heat shock 88 72 912 protein HtpX
 [Streptococcus gordonii] 107 2 219 962 gnl.vertline.PID.vertline.e339862 putative
 acylneuraminate lyase 88 75 744 [Clostridium tertium] 111 8 14073 10420
 gi.vertline.402363 RNA polymerase beta-subunit 88 74 3654 [Bacillus subtilis] 126 9
 13096 12062 gnl.vertline.PID.vertline.e311468 unknown [Bacillus subtilis] 88 74
 1035 140 17 19143 18874 gl.vertline.1573659 H. influenzae predicted coding 88 61
 270 region HI0659 [Haemophilus influenzae] 144 1 394 555
 gnl.vertline.PID.vertline.e274705 lactate oxidase [Streptococcus 88 75 162 iniae]
 148 4 2723 3493 gi.vertline.1591672 phosphate transport 88 68 771 system ATP-
 binding protein [Methanococcus jannaschii] 160 8 5853 6278 gi.vertline.1773267
 ATPase, epsilon subunit 88 65 426 [Streptococcus mutans] 177 4 1770 2885
 gi.vertline.149426 putative [Lactococcus lactis] 88 72 1116 211 6 4140 3613
 gi.vertline.535273 aminopeptidase C [Streptococcus 88 74 528 thermophilus] 231 4
 580 957 gi.vertline.40186 homologous to E. coli ribosomal 88 78 378 protein L27
 [Bacillus subtilis] 260 5 2387 2998 gi.vertline.1196922 unknown protein [Insertion
 88 69 612 sequence IS861] 291 6 2017 3375 gnl.vertline.PID.vertline.d100571
 adenylosuccinate synthetase 88 75 1359 [Bacillus subtilis] 319 4 658 317
 gi.vertline.603578 serine/threonine kinase 88 88 342 [Phytophthora capsici] 40 5
 4353 4514 gi.vertline.153672 lactose repressor 87 56 162 [Streptococcus mutans] 49
 10 10660 10929 gi.vertline.1196921 unknown protein [Insertion 87 72 270 sequence
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 6623 7039 gi.vertline.1044978 ribosomal protein S8 87 73 417 [Bacillus subtilis] 75
 8 5411 6625 gi.vertline.1877422 galactokinase 87 78 1215 [Streptococcus mutans] 80
 2 703 2805 gni.vertline.pid.vertline.d101166 elongation factor G 87 76 2103
 [Bacillus subtilis] 82 1 541 248 gi.vertline.1196921 unknown protein 87 69 294
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 phenylalany-tRNA synthetase 87 74 1137 beta subunit [Bacillus subtilis] 214 14
 10441 8516 gi.vertline.2281305 glucose inhibited division 87 75 1926 protein
 homolog GidA [Lactococcus lactis cremoris] 220 2 2742 874
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 factor EF-G [Bacillus subtilis] 260 4 2096 2389 gi.vertline.1196921 unknown protein
 87 72 294 [Insertion sequence IS861] 323 1 27 650 gi.vertline.897795 30S ribosomal
 protein 87 73 624 [Pediococcus acidilactici] 357 1 154 570 gi.vertline.1044978

ribosomal protein S8 87 73 417 [Bacillus subtilis] 49 11 10927 11445
gi.vertline.1196922 unknown protein 86 63 519 [Insertion sequence IS861] 59 12 7461
9224 gi.vertline.951051 relaxase [Streptococcus 86 68 1764 pneumoniae] 65 4 1553
2401 pir.vertline.A02759.vertline.R5- BS ribosomal protein L2 - 86 77 849 Bacillus
stearotherophilus 65 23 10957 11610 gi.vertline.44074 adenylate kinase 86 76 654
[Lactococcus lactis] 82 4 4374 4856 gi.vertline.153745 mannitol-specific enzyme 86
72 483 III [Streptococcus mutans] 102 4 4270 4986 gnl.vertline.PID.vertline.e-
264705 OMP decarboxylase 86 76 717 [Lactococcus lactis] 106 6 7824 6880
gnl.vertline.PID.vertline.el37598 aspartate transcarbamylase 86 68 945
[Lactobacillus leichmannii] 107 1 1 273 gnl.vertline.PID.vertline.e339862 putative
acylneuraminate 86 71 273 lyase [Clostridium tertium] 111 7 10432 6710
gnl.vertline.PID.vertline.e228283 DNA-dependent RNA polymerase 86 80 3723
[Streptococcus pyogenes] 131 9 5704 4892 gi.vertline.1661193 polipoprotein
diacylglycerol 86 71 813 transferase [Streptococcus mutans] 134 7 6430 7980
gi.vertline.2388637 glycerol kinase 86 73 1551 [Enterococcus faecalis] 146 11 7473
6583 gi.vertline.1591731 melvalonate kinase 86 72 891 [Methanococcus jannaschii]
153 2 595 2010 gi.vertline.2160707 dipeptidase 86 78 1416 [Lactococcus lactis] 154
1 2 1435 gi.vertline.1857246 6-phosphogluconate dehydrogenase 86 74 1434
[Lactococcus lactis] 161 5 5025 6284 gi.vertline.47529 Unknown [Streptococcus
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glyceraldehyde- 86 73 1482 3-phosphate dehydrogenase [Streptococcus mutans] 210 8
3659 6571 gi.vertline.153661 translational initiation factor IF2 86 76 2913
[Enterococcus faecium] 250 1 2 187 gi.vertline.1573551 asparagine synthetase A
(asnA) 86 68 186 [Haemophilus influenzae] 36 4 2644 3909 gi.vertline.2149909 cell
division protein [Enterococcus 85 73 1266 faecalis] 38 4 2475 3587
gi.vertline.2058545 putative ABC transporter subunit 85 72 1113 ComYB
[Streptococcus gordonii] 38 5 3577 3915 gi.vertline.2058546 ComYC [Streptococcus
gordonii] 85 80 339 57 5 2797 3789 gnl.vertline.PID.vertline.dl01316 YqfJ [Bacillus
subtilis] 85 72 993 82 5 4915 6054 gi.vertline.153746 mannitol-phosphate
dehydrogenase 85 68 1140 [Streptococcus mutans] 83 15 14690 15793
gi.vertline.143371 phosphoribosyl aminoimidazole 85 69 1104 synthetase (PUR-M)
[Bacillus subtilis] 87 2 1417 2388 gi.vertline.1184967 ScrR [Streptococcus mutans]
85 69 972 108 3 2666 3154 gi.vertline.153566 ORF (19K protein) [Enterococcus 85 67
489 faecalis] 127 2 312 692 gi.vertline.1044989 ribosomal protein S13 85 72 381
[Bacillus subtilis] 128 3 1534 2409 gi.vertline.1685110 tetrahydrofolate
dehydrogenase/ 85 71 876 cyclohydrolase [Streptococcus thermophilus] 137 7 2962
4767 gnl.vertline.PID.vertline.dl00347 Na⁺-ATPase alpha subunit 85 74 1806
[Enterococcus hirae] 170 2 2622 709 gnl.vertline.PID.vertline.dl02006 (AB001488)
FUNCTION UNKNOWN, 85 70 1914 SIMILAR PRODUCT IN E COLI, H. INFLUENZAE AND NEISSERIA
MENINGITIDIS. [Bacillus subtilis] 187 5 3760 4386 gi.vertline.727436 putative 20-
kDa protein 85 65 627

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L2: Entry 8 of 35

File: PGPB

Feb 12, 2004

DOCUMENT-IDENTIFIER: US 20040029118 A1

TITLE: Streptococcus pneumoniae polynucleotides and sequences

Detail Description Table CWU:

181 8 4033 5751 gi.vertline.149411 enzyme III [Lactococcus lactis] 89 80 1719 211 4
 3149 2793 gi.vertline.535273 aminopeptidase C 89 83 357 [Streptococcus
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[Lactococcus lactis] 161 5 5025 6284 gi.vertline.47529 Unknown [Streptococcus
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[Enterococcus faecium] 250 1 2 187 gi.vertline.1573551 asparagine synthetase A
(asnA) 86 68 186 [Haemophilus influenzae] 36 4 2644 3909 gi.vertline.2149909 cell
division protein [Enterococcus 85 73 1266 faecalis] 38 4 2475 3587
gi.vertline.2058545 putative ABC transporter subunit 85 72 1113 ComYB
[Streptococcus gordonii] 38 5 3577 3915 gi.vertline.2058546 ComYC [Streptococcus
gordonii] 85 80 339 57 5 2797 3789 gnl.vertline.PID.vertline.d101316 YqfJ [Bacillus
subtilis] 85 72 993 82 5 4915 6054 gi.vertline.153746 mannitol-phosphate
dehydrogenase 85 68 1140 [Streptococcus mutans] 83 15 14690 15793
gi.vertline.143371 phosphoribosyl aminoimidazole 85 69 1104 synthetase (PUR-M)
[Bacillus subtilis] 87 2 1417 2388 gi.vertline.1184967 ScrR [Streptococcus mutans]
85 69 972 108 3 2666 3154 gi.vertline.153566 ORF (19K protein) [Enterococcus 85 67
489 faecalis] 127 2 312 692 gi.vertline.1044989 ribosomal protein S13 85 72 381
[Bacillus subtilis] 128 3 1534 2409 gi.vertline.1685110 tetrahydrofolate
dehydrogenase/ 85 71 876 cyclohydrolase [Streptococcus thermophilus] 137 7 2962
4767 gnl.vertline.PID.vertline.d100347 Na⁺ -ATPase alpha subunit 85 74 1806
[Enterococcus hirae] 170 2 2622 709 gnl.vertline.PID.vertline.d102006 (AB001488)
FUNCTION UNKNOWN, 85 70 1914 SIMILAR PRODUCT IN E COLI, H. INFLUENZAE AND NEISSERIA
MENINGITIDIS. [Bacillus subtilis] 187 5 3760 4386 gi.vertline.727436 putative 20-
kDa protein 85 65 627

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Mar 14, 2002

TITLE: STREPTOCOCCUS PNEUMONIAE POLYNUCLEOTIDES AND SEOUENCES

231 4 580 957 gi.vertline.40186 homologous to E.coli ribosomal protein L27
[Bacillus subtilis] 88 78 378 260 5 2387 2998 gi.vertline.1196922 unknown protein
[Insertion sequence IS861] 88 69 612 291 6 2017 3375
gnl.vertline.PID.vertline.dl00571 adenylosuccinate synthetase [Bacillus subtilis]
88 75 1359 319 4 658 317 gi.vertline.603578 serine/threonine kinase [Phytophthora
capsici] 88 88 342 40 5 4353 4514 gi.vertline.153672 lactose repressor
[Streptococcus mutans] 87 56 162 49 10 10660 10929 gi.vertline.1196921 unknown
protein [Insertion sequence IS861] 87 72 270 65 7 3140 3808 gi.vertline.1165309 S3
[Bacillus subtilis] 87 73 669 65 15 6623 7039 gi.vertline.1044978 ribosomal protein
S8 [Bacillus subtilis] 87 73 417 75 8 5411 6625 gi.vertline.1877422 galactokinase
[Streptococcus mutans] 87 78 1215 80 2 703 2805 gnl.vertline.PID.vertline.dl01166
elongation factor G [Bacillus subtilis] 87 76 2103 82 1 541 248 gi.vertline.1196921
unknown protein [Insertion sequence IS861] 87 69 294 140 23 25033 23897
gnl.vertline.PID.vertline.e254999 phenylalanyl-tRNA synthetase beta subunit
[Bacillus subtilis] 87 74 1137 214 14 10441 8516 gi.vertline.2281305 glucose
inhibited division protein homolog GidA 87 75 1926 [Lactococcus lactis cremoris]
220 2 2742 874 gnl.vertline.PID.vertline.e324358 product highly similar to
elongation factor EF-G 87 73 1869 [Bacillus subtilis] 260 4 2096 2389
gi.vertline.1196921 unknown protein [Insertion sequence IS861] 87 72 294 323 1 27
650 gi.vertline.897795 30S ribosomal protein [Pediococcus acidilactici] 87 73 624
357 1 154 570 gi.vertline.1044978 ribosomal protein S8 [Bacillus subtilis] 87 73
417 49 11 10927 11445 gi.vertline.1196922 unknown protein [Insertion sequence
IS861] 86 63 519 59 12 7461 9224 gi.vertline.951051 relaxase [Streptococcus
pneumoniae] 86 68 1764 65 4 1553 2401 pir.vertline.A02759.vertline.R5BS ribosomal
protein L2 - Bacillus stearothermophilus 86 77 849 65 23 10957 11610
gi.vertline.44074 adenylate kinase [Lactococcus lactis] 86 76 6541 82 4 4374 4856
gi.vertline.153745 mannitol-specific enzyme III [Streptococcus mutans] 86 72 483
102 4 270 4986 gnl.vertline.PID.vertline.e264705 CMP decarboxylase [Lactococcus
lactis] 86 76 717 106 6 7824 6880 gnl.vertline.PID.vertline.el37598 aspartate
transcarbamylase [Lactobacillus leichmannii] 86 68 945 107 1 1 273
gnl.vertline.PID.vertline.e339862 putative acylneuraminate lyase [Clostridium
tertiula] 86 71 273 111 7 10432 6710 gnl.vertline.PID.vertline.e228283 DNA-
dependent RNA polymerase [Streptococcus pyogenes] 86 80 3723 131 9 5704 4892
gi.vertline.1661193 polipoprotein diacylglycerol transferase [Streptococcus mutans]
86 71 813 134 7 6430 7980 gi.vertline.2388637 glycerol kinase [Enterococcus
faecalis] 86 73 1551 146 11 7473 6583 gi.vertline.1591731 melvalonate kinase
[Methanococcus jannaschii] 86 72 891 153 2 595 2010 gi.vertline.2160707 dipeptidase
[Lactococcus lactis] 86 78 1416 154 1 2 1435 gi.vertline.1857246 6-phosphogluconate
dehydrogenase [Lactococcus lactis] 86 74 1434 161 5 5025 6284 gi.vertline.47529
Unknown [Streptococcus selivarius] 86 66 1260 184 1 2 1483 gi.vertline.642667 NADP-
dependent glyceraldehyde-3-phosphate dehydrogenase 86 73 1482 [Streptococcus
mutans] 210 8 3659 6571 gi.vertline.153661 translational initiation factor IF2
[Enterococcus faecium] 86 76 2913 250 1 2 187 gi.vertline.1573551 asparagine
synthetase A (asnA) [Haemophilus influenzae] 86 68 186 36 4 2644 3909
gi.vertline.2149909 cell division protein [Enterococcus faecalis] 85 73 1266 38 4
2475 3587 gi.vertline.2058545 putative ABC transporter subunit ComYB 85 72 1113

[Streptococcus gordonii] 38 5 3577 3915 gi.vertline.2058546 ComYC [Streptococcus gordonii] 85 80 339 57 5 2797 3789 gnl.vertline.PID.vertline.d1013- 16 YgfJ [Bacillus subtilis] 85 72 993 82 5 4915 6054 gi.vertline.153746 mannitol-phosphate dehydrogenase [Streptococcus isutens] 85 68 1140 83 15 14690 15793 gi.vertline.143371 phosphoribosyl aminoimideazole synthetase (PUR-M) 85 69 1104 [Bacillus subtilis] 87 2 1417 2388 gi.vertline.184967 ScrR [Streptococcus mutans] 85 69 972 108 3 2666 3154 gi.vertline.153566 ORF (19K protein) [Enterococcus faecalis] 85 67 489 127 2 312 692 gi.vertline.1044989 ribosomal protein S13 [Bacillus subtilis] 85 72 381 128 3 1534 2409 gi.vertline.1685110 tetrahydrofolate dehydrogenase/cyclohydrolase 85 71 876 [Streptococcus thermophilus] 137 7 2962 4767 gnl.vertline.PID.vertline.d100347 Na⁺ -ATPase alpha subunit [Enterococcus hirae] 85 74 1806 170 2 2622 709 gnl.vertline.PID.vertline.d102006 (AF001488) FUNCTION UNKNOWN, 85 70 1914 SIMILAR PRODUCT IN E.COLI, N. INFLUENZAE AND NEISSERIA MENINGITIDIS. [Bacillus subtilis] 187 5 3760 4386 gi.vertline.727436 putative 20-kDa protein [Lactococcus lactis] 85 65 627 233 2 728 1873 gi.vertline.1163116 ORF-5 [Streptococcus pneumoniae] 85 67 1146 234 3 962 1255 gi.vertline.2293155 (AF008220) YtiA [Bacillus subtilis] 85 61 294 240 1 309 1931 gi.vertline.143597 CTP synthetase [Bacillus subtilis] 85 70 1623 6 1 199 1521 gi.vertline.508979 GTP-binding protein [Bacillus subtilis] 84 72 1323 10 4 4375 3443 gnl.vertline.PID.vertline.e339862 putative ecylneureminate lyase [Clostridium tertium] 84 70 933 14 1 63 2093 gi.vertline.520753 DNA topoisomerase I [Bacillus subtilis] 84 69 2031 19 4 1793 2593 gi.vertline.2352484 (AF005098) RNaseH II [Lactococcus lactis] 84 68 801 20 17 17720 19687 gnl.vertline.PID.vertline.d100584 cell division protein [Bacillus subtilis] 84 71 1968 22 28 21723 20884 gi.vertline.299163 alanine dehydrogenase [Bacillus subtilis] 84 68 840 30 10 7730 6792 gnl.vertline.PID.vertline.d100296 fructokinase [Streptococcus mutans] 84 75 939 33 9 5650 5300 gi.vertline.147194 phnA protein [Escherichia coli] 84 71 351 36 22 21551 20772 gi.vertline.3106311 ATP binding protein [Streptococcus gordonii] 84 72 780 48 4 2837 2505 gi.vertline.8826D9 6-phospho-beta-glucosidase [Escherichia coli] 84 69 333 58 1 41 1518 gi.vertline.450849

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File: PGPB

Nov 1, 2001

DOCUMENT-IDENTIFIER: US 20010036636 A1

TITLE: Biochemical method to measure niacin status in a biological sample

Detail Description Paragraph:

[0062] Other enzyme, enzyme substrate pairs are well known to those of skill in the art and may be found by consultation with standard biochemistry references.. Examples of suitable NAD dependent (i.e., NAD specific) enzymes and substrate pairs include alcohol dehydrogenase and ethanol; malate dehydrogenase and malate; lactate dehydrogenase and lactate; NAD specific isocitrate dehydrogenase (cytoplasmic) and isocitrate; and glyceraldehyde-3-phosphate dehydrogenase and glyceraldehyde-3-phosphate. Examples of suitable NADP dependent enzymes and enzyme substrate pairs include glucose-6-phosphate dehydrogenase and glucose-6-phosphate; 6-phosphogluconate dehydrogenase and 6-phosphogluconate; malic enzyme and malate; NADP specific isocitrate dehydrogenase (mitochondrial) and isocitrate.

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